



PCT

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RAW SEQUENCE LISTING

DATE: 04/15/2003

PATENT APPLICATION: US/09/889,733B

TIME: 13:51:10

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\04152003\I889733B.raw

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2 <110> APPLICANT: VALLANCE, Patrick
3     LEIPER, James
4     WHITLEY, Guy
5     CHARLES, Ian
7 <120> TITLE OF INVENTION: DIMETHYLARGININE DIMETHYLAMINOHYDROLASES
9 <130> FILE REFERENCE: 117-358
11 <140> CURRENT APPLICATION NUMBER: US 09/889,733B
12 <141> CURRENT FILING DATE: 2001-09-14
14 <150> PRIOR APPLICATION NUMBER: GB 99017505.5
15 <151> PRIOR FILING DATE: 1999-01-26
16 <150> PRIOR APPLICATION NUMBER: GB 9913066.8
17 <151> PRIOR FILING DATE: 1999-06-04
19 <160> NUMBER OF SEQ ID NOS: 43
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 858
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(858)
32 <400> SEQUENCE: 1
33 atg gcc ggc ctc ggc cac ccc tcc gcc ttc ggc cgg gcc acc cac gcc      48
34 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
35 1          5          10          15
37 gtg gtg cgg gcg cta ccc gag tcg ctc tgc cag cac gcg ctg aga agc      96
38 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
39          20          25          30
41 gcc aag ggc gag gag gtg gac gtc gcc cgc gcg gaa cgg cag cac cag      144
42 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
43          35          40          45
45 ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag      192
46 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
47          50          55          60
49 ctg ccg gcc gac gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg      240
50 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
51 65          70          75          80
53 gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg gcg ccg      288
54 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
55          85          90          95
57 agc cgg agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt      336
58 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
59          100          105          110

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61 cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc      384
62 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
63      115      120      125
65 gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa      432
66 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
67      130      135      140
69 agg aca aat caa cga ggt gct gaa atc ttg gct gat act ttt aag gac      480
70 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
71 145      150      155      160
73 tat gca gtc tcc aca gtg cca gtg gca gat ggg ttg cat ttg aag agt      528
74 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
75      165      170      175
77 ttc tgc agc atg gct ggg cct aac ctg atc gca att ggg tct agt gaa      576
78 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
79      180      185      190
81 tct gca cag aag gcc ctt aag atc atg caa cag atg agt gac cac cgc      624
82 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
83      195      200      205
85 tac gac aaa ctc act gtg cct gat gac ata gca gca aac tgt ata tat      672
86 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
87      210      215      220
89 cta aat atc ccc aac aaa ggg cac gtc ttg ctg cac cga acc ccg gaa      720
90 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
91 225      230      235      240
93 gag tat cca gaa agt gca aag gtt tat gag aaa ctg aag gac cat atg      768
94 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
95      245      250      255
97 ctg atc ccc gtg agc atg tct gaa ctg gaa aag gtg gat ggg ctg ctc      816
98 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
99      260      265      270
101 acc tgc tgc tca gtt tta att aac aag aag gta gac tcc tga      858
102 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
103      275      280      285
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 285
107 <212> TYPE: PRT
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 2
111 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
112 1      5      10      15
115 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
116      20      25      30
118 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
119      35      40      45
121 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
122      50      55      60
124 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
125 65      70      75      80
127 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro

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128          85          90          95
130 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
131          100          105          110
133 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
134          115          120          125
136 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
137          130          135          140
139 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
140 145          150          155          160
142 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
143          165          170          175
145 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
146          180          185          190
148 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
149          195          200          205
151 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
152          210          215          220
154 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
155 225          230          235          240
157 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
158          245          250          255
160 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
161          260          265          270
163 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
164          275          280          285
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 858
168 <212> TYPE: DNA
169 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (1)..(858)
175 <400> SEQUENCE: 3
176 atg ggg acg ccg ggg gag ggg ctg ggc cgc tgc tcc cat gcc ctg atc      48
177 Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
178 1          5          10          15
180 cgg gga gtc cca gag agc ctg gcg tcg ggg gaa ggt gcg ggg gct ggc      96
181 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
182          20          25          30
184 ctt ccc gct ctg gat ctg gcc aaa gct caa agg gag cac ggg gtg ctg      144
185 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
186          35          40          45
188 gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca      192
189 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
190          50          55          60
192 cct gag gag tca ttg ccg ctg gga ccg ctg ctt ggc gac acg gcc gtg      240
193 Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
194 65          70          75          80
196 atc caa ggg gac acg gcc cta atc acg cgg ccc tgg agc ccc gct cgt      288

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197 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
198      85      90      95
200 agg cca gag gtc gat gga gtc cgc aaa gcc ctg caa gac ctg ggg ctc      336
201 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
202      100      105      110
204 cga att gtg gaa ata gga gac gag aac gcg acg ctg gat ggc act gac      384
205 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
206      115      120      125
208 gtt ctc ttc acc ggc cgg gag ttt ttc gta ggc ctc tcc aaa tgg acc      432
209 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
210      130      135      140
212 aat cac cga gga gct gag atc gtg gcg gac acg ttc cgg gac ttc gcc      480
213 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
214 145      150      155      160
216 gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc      528
217 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
218      165      170      175
220 ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc      576
221 Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
222      180      185      190
224 caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc      624
225 Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
226      195      200      205
229 tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt      672
230 Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg
231      210      215      220
233 cct ggg ttg cct ggt gtg ccc cct ttc ctc ctg cac cgt gga ggt ggg      720
234 Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
235 225      230      235      240
237 gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc      768
238 Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
239      245      250      255
241 ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc      816
242 Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
243      260      265      270
245 agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga      858
246 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
247      275      280      285
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 285
252 <212> TYPE: PRT
253 <213> ORGANISM: Homo sapiens
255 <400> SEQUENCE: 4
256 Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
257 1      5      10      15
259 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
260      20      25      30
262 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
263      35      40      45

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265 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
266      50      55      60
268 Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
269 65      70      75      80
271 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
272      85      90      95
274 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
275      100     105     110
277 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
278      115     120     125
280 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
281      130     135     140
283 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
284 145      150     155     160
286 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
287      165     170     175
289 Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
290      180     185     190
292 Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
293      195     200     205
295 Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg
296      210     215     220
298 Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
299 225      230     235     240
301 Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
302      245     250     255
304 Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
305      260     265     270
307 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
308      275     280     285

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310 <210> SEQ ID NO: 5

311 <211> LENGTH: 777

312 <212> TYPE: DNA

313 <213> ORGANISM: S. coelicolor

315 <220> FEATURE:

316 <221> NAME/KEY: CDS

317 <222> LOCATION: (1)..(777)

319 <400> SEQUENCE: 5

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320 gtg ccc agc aag aag gcc ctg gtc cgc cgc ccc agc ccc agg ctc gcc      48
321 Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala
322 1      5      10      15
324 gaa gga ctg gtg aca cac gtc gag cgg gag cag gtc gat cac ggc ctg      96
325 Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
326      20      25      30
328 gcc ctc gaa cag tgg gac gcc tac gtc gag gcc ctc gga gca cac ggc      144
329 Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
330      35      40      45
332 tgg gag act ctg gag gtg gac ccg gcc gag tac tgt ccg gac tcg gtc      192
333 Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val

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VERIFICATION SUMMARY

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